

What is claimed is:

1. A method for determining whether a HIV-1 has an increased likelihood of being hypersusceptible to treatment with a protease inhibitor, comprising: detecting whether the protease encoded by said HIV exhibits the presence or absence of a mutation associated with hypersusceptibility to treatment with said protease inhibitor at amino acid position 16, 20, 33, 36, 37, 39, 45, 65, 69, 77, 89 or 93 of an amino acid sequence of said protease, wherein the presence of said mutation indicates that the HIV has an increased likelihood of being hypersusceptible to treatment with the protease inhibitor, with the proviso that said mutation is not L33F.
2. The method of claim 1, wherein the protease has a sequence that is greater than 80% identical to SEQ ID NO:1.
3. A method for determining whether an individual infected with HIV-1 has an increased likelihood of being hypersusceptible to treatment with a protease inhibitor, comprising detecting, in a sample from said individual, the presence or absence of a mutation associated with hypersusceptibility to treatment with said protease inhibitor at amino acid position 16, 20, 33, 36, 37, 39, 45, 65, 69, 77, 89 or 93 of the amino acid sequence of the protease of the HIV-1, wherein the presence of said mutation indicates that the individual has an increased likelihood of being hypersusceptible to treatment with the protease inhibitor, with the proviso that said mutation is not L33F.
4. The method of claim 3, wherein the protease has a sequence that is greater than 80% identical to SEQ ID NO:1.
5. An isolated oligonucleotide between about 10 and about 40 nucleotides long encoding a portion of an HIV protease that comprises a mutation at amino acid position 16, 20, 33, 36, 37, 39, 45, 65, 69, 77, 89 or 93 of an amino acid sequence of said protease in said human immunodeficiency virus, wherein the mutation is associated with hypersusceptibility to a protease inhibitor, with the proviso that said mutation is not L33F.
- 30 6. The method of claim 1, wherein said protease inhibitor is amprenavir.
7. The method of claim 6, wherein said amino acid position is 20, 36, 39, 65, 69, 77 or 89.

8. The method of claim 1, wherein said protease inhibitor is indinavir.
9. The method of claim 8, wherein said amino acid position is 16, 39 or 65.
10. The method of claim 1, wherein said protease inhibitor is nelfinavir.
11. The method of claim 10, wherein said amino acid position is 16, 39, 65, 69 or 89.
- 5 12. The method of claim 1, wherein said protease inhibitor is ritonavir.
13. The method of claim 12, wherein said amino acid position is 39, 65 or 93.
14. The method of claim 1, wherein said protease inhibitor is saquinavir.
15. The method of claim 14, wherein said amino acid position is 33, 37, 45, 65 or 77, with the proviso that the mutation at amino acid position 33 is not 33F.
- 10 16. The method of claim 1, wherein said protease inhibitor is lopinavir.
17. The method of claim 16, wherein said amino acid position is 33, 39, 65, 77 or 93, with the proviso that the mutation at amino acid position 33 is not 33F.
18. The method of claim 3, wherein the individual is undergoing or has undergone prior treatment with an anti-viral drug.
- 15 19. The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with hypersusceptibility to treatment with said protease inhibitor at at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 of the amino acid positions.
- 20 20. A method for determining whether a HIV-1 has a decreased likelihood of being hypersusceptible to a protease inhibitor, comprising: detecting whether the protease encoded by said HIV-1 exhibits the presence or absence of a mutation negatively associated with hypersusceptibility to said protease inhibitor at amino acid position 10, 15, 36, 41, 57, 60, 63, 71 or 93 of an amino acid sequence of said protease, wherein the presence of said mutation indicates that the HIV has a decreased likelihood of being hypersusceptible to the protease inhibitor.
- 25 21. A method for determining whether an individual infected with HIV-1 has a decreased likelihood of being hypersusceptible to treatment with a protease inhibitor, comprising detecting, in a sample from said individual, the presence or absence of a mutation negatively associated with hypersusceptibility to treatment with said protease inhibitor at amino acid position 10, 15, 36, 41, 57, 60, 63, 71 or

93 of the amino acid sequence of the protease of the HIV-1, wherein the presence of said mutation indicates that the individual has a decreased likelihood of being hypersusceptible to treatment with the protease inhibitor.